Amendment to the specification:

Insert the paper copy of the Sequence Listing filed herewith following the Drawings.

Replace the paragraph beginning at page 38, line 11 with the following rewritten paragraph:

Double-stranded DNA oligonucleotides having, on one strand, nucleotide sequences AAATTATATTAT (SEQ ID NO:1) (peak 1) and GGGCCGCGCCGC (SEQ ID NO:2) (peak 2) are incubated in the presence of netropsin, a well-documented AT-selective binder. At r0, the two strands are present without any of the drug. At r1, the presence of netropsin (20 μM) causes a new peak (the complex of netropsin and the AT dodecamer) to appear in the trace. Increasing the amount of netropsin in the mixture to 40 μM (r2) causes complete conversion of the free AT dodecamer to its complex with netropsin.

Replace the paragraph beginning at page 38, line 20 with the following rewritten paragraph:

From the traces shown in Figure 1, it can be determined that:

(i) netropsin is AT selective; and

(ii) it has a binding ratio of 2:1 (drug : DNA) with AAATTATATTAT (SEQ ID NO:1) (1 drug molecule to each available binding site).

Replace the paragraph beginning at page 38, line 25 with the following rewritten paragraph:

Figure 2: Binding studies with 12/41 (the compound of Example 2)
Compound 12/41 shows, with AAATTATATTAT (SEQ ID NO:1), the same 2:1 binding ratio as netropsin (as well as similar AT-selectivity).

Replace the paragraph beginning at page 39, line 1 with the following rewritten paragraph:

Figure 3: Binding studies with 13/20 (the compound of Example 3)

Figure 3 presents the binding electropherograms of 13/20 in the presence of a double-stranded DNA decamer having, on one strand, the nucleotide sequence CGACTAGTCG (SEQ ID NO:3), the central part of which was indicated to be a high affinity binding site from footprinting studies (see Figure 7). Here we see that the binding ratio is 4:1 (drug : DNA). This result demonstrates that 13/20 has a strong affinity for the given sequence, and also that the minor groove produced by the DNA decamer accommodates 4 drug-binding molecules in one binding site.

Replace the paragraph beginning at page 39, line 11 with the following rewritten paragraph:

Figure 4: Binding studies with distamycin

Figure 4 presents the binding electropherograms of the well-known compound distamycin in the presence of the double-stranded DNA decamer having, on one strand, the nucleotide sequence CGACTAGTCG (SEQ ID NO:3). It can clearly be seen, distamycin has no affinity for the CGACTAGTCG (SEQ ID NO:3) sequence even at a drug to DNA ratio of 4:1 (the trace labelled r4).

Replace the paragraph beginning at page 39, line 18 with the following rewritten paragraph:

Figure 5: Competitive binding studies with compound 13/20

Figure 5 presents the binding electropherograms for 13/20 in the presence of a mixture of double-stranded DNA oligonucleotides, one having, on one strand, the dodecameric nucleotide sequence AAATTATATTAT (SEQ ID NO:1) (peak 1) and the other having, on one strand, the decameric nucleotide sequence GGACTAGTCG (SEQ ID NO:4) (peak 2). It can be seen from the results that 13/20 has a greater affinity for the decamer ACTA sequence (as indicated by the earlier disappearance of the peak corresponding to the uncomplexed ACTA sequence).

Replace the paragraph beginning at page 39, line 28 with the following rewritten paragraph:

Figure 6: Further binding studies with compound 13/20

Figure 6 presents the binding electropherograms of 13/20 incubated against the double-stranded DNA oligonucleotide having, on one strand, the decameric nucleotide sequence CCACTAGTGG (SEQ ID NO:5). The result obtained for this binding was identical with that achieved with the sequence in Fig. 3, showing that it is the central sequence which dominates binding, as indicated by footprinting.

Replace the paragraph beginning at page 40, line 6 with the following rewritten paragraph:

Figures 7 and 8: DNA footprinting studies

DNA footprinting is a well-established technique in which a section of radio-labelled DNA (SEQ ID NO:6) is incubated with a chemical or biological cleaving agent, in the presence and absence of a putative binding ligand. Regions of ligand binding will show as blanks in the 'ladder'. Knowing the DNA sequence, the binding sites can then be deduced, from the location of these blanks.